

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/663,497A
Source: IFW
Date Processed by STIC: 3-17-06

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 03/17/2006

PATENT APPLICATION: US/10/663,497A

TIME: 13:42:16

Input Set : D:\seqlist.txt

Output Set: N:\CRF4\03172006\J663497A.raw

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4 <110> APPLICANT: Dale Umetsu
5     Rosemarie DeKruyff
6     Jennifer McIntire
7     Gordon Freeman
9 <120> TITLE OF INVENTION: T CELL REGULATORY GENES ASSOCIATED WITH
10    IMMUNE DISEASE
12 <130> FILE REFERENCE: STAN-235CIP
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/663,497A
C--> 14 <141> CURRENT FILING DATE: 2003-09-15
14 <150> PRIOR APPLICATION NUMBER: 60/302,344
15 <151> PRIOR FILING DATE: 2001-06-29
17 <150> PRIOR APPLICATION NUMBER: 10/188,012
18 <151> PRIOR FILING DATE: 2002-07-01
20 <160> NUMBER OF SEQ ID NOS: 53
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 305
26 <212> TYPE: PRT
27 <213> ORGANISM: M. musculus
29 <220> FEATURE:
30 <221> NAME/KEY: VARIANT
31 <222> LOCATION: (1)...(305)
32 <223> OTHER INFORMATION: TIM-1 BALB/c allele
34 <400> SEQUENCE: 1
35 Met Asn Gln Ile Gln Val Phe Ile Ser Gly Leu Ile Leu Leu Pro
36 1           5           10           15
37 Gly Thr Val Asp Ser Tyr Val Glu Val Lys Gly Val Val Gly His Pro
38           20           25           30
39 Val Thr Leu Pro Cys Thr Tyr Ser Thr Tyr Arg Gly Ile Thr Thr Thr
40           35           40           45
41 Cys Trp Gly Arg Gly Gln Cys Pro Ser Ser Ala Cys Gln Asn Thr Leu
42           50           55           60
43 Ile Trp Thr Asn Gly His Arg Val Thr Tyr Gln Lys Ser Ser Arg Tyr
44 65           70           75           80
45 Asn Leu Lys Gly His Ile Ser Glu Gly Asp Val Ser Leu Thr Ile Glu
46           85           90           95
47 Asn Ser Val Glu Ser Asp Ser Gly Leu Tyr Cys Cys Arg Val Glu Ile
48           100          105          110
49 Pro Gly Trp Phe Asn Asp Gln Lys Val Thr Phe Ser Leu Gln Val Lys
50           115          120          125
51 Pro Glu Ile Pro Thr Arg Pro Pro Thr Arg Pro Thr Thr Arg Pro
52           130          135          140
53 Thr Ala Thr Gly Arg Pro Thr Thr Ile Ser Thr Arg Ser Thr His Val

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54 145          150          155          160
55 Pro Thr Ser Ile Arg Val Ser Thr Ser Thr Pro Pro Thr Ser Thr His
56          165          170          175
57 Thr Trp Thr His Lys Pro Glu Pro Thr Thr Phe Cys Pro His Glu Thr
58          180          185          190
59 Thr Ala Glu Val Thr Gly Ile Pro Ser His Thr Pro Thr Asp Trp Asn
60          195          200          205
61 Gly Thr Val Thr Ser Ser Gly Asp Thr Trp Ser Asn His Thr Glu Ala
62          210          215          220
63 Ile Pro Pro Gly Lys Pro Gln Lys Asn Pro Thr Lys Gly Phe Tyr Val
64 225          230          235          240
65 Gly Ile Cys Ile Ala Ala Leu Leu Leu Leu Leu Val Ser Thr Val
66          245          250          255
67 Ala Ile Thr Arg Tyr Ile Leu Met Lys Arg Lys Ser Ala Ser Leu Ser
68          260          265          270
69 Val Val Ala Phe Arg Val Ser Lys Ile Glu Ala Leu Gln Asn Ala Ala
70          275          280          285
71 Val Val His Ser Arg Ala Glu Asp Asn Ile Tyr Ile Val Glu Asp Arg
72          290          295          300
73 Pro
74 305
77 <210> SEQ ID NO: 2
78 <211> LENGTH: 918
79 <212> TYPE: DNA
80 <213> ORGANISM: Mus musculus
82 <400> SEQUENCE: 2
83 atgaatcaga ttcaagtctt catttcaggc ctcatactgc ttctcccagg cactgtggat 60
84 tccttatgtg aagtaaaggg ggtagtgggt caccctgtca cacttccatg tacttactca 120
85 acatatcgtg gaatcacaaac gacatggttg ggccgagggc aatgcccac tctgtgtgt 180
86 caaaatacac ttatttggac caatggacat cgtgtcacct atcagaagag cagtcggtac 240
87 aacttaaagg ggcataatttc agaaggagat gtgtccttga cgatagagaa ctctgttgag 300
88 agtgacagtg gtctgtattg ttgtcgagtg gagattcctg gatgggttaa tgatcagaaa 360
89 gtgacctttt cattgcaagt taaaccagag attcccacac gtcctccaac aagaccacac 420
90 actacaaggc ccacagctac aggaagaccc acgactattt caacaagatc cacacatgta 480
91 ccaacatcaa tcagagtctc tacctccact cctccaacat ctacacacac atggactcac 540
92 aaaccagaac ccactacatt ttgtcccat gagacaacag ctgaggtgac aggaatccca 600
93 tcccatactc ctacagactg gaatggcact gtgacatcct caggagatac ctggagtaat 660
94 cacactgaag caatccctcc aggggaagccg cagaaaaacc ctactaaggg cttctatgtt 720
95 ggcactctgca tcgcagccct gctgctactg ctccttgtga gcaccgtggc tatcaccagg 780
96 tacatactta tgaaaaggaa gtcagcatct ctaagcgtgg ttgccttccg tgtctctaag 840
97 attgaagctt tgcagaacgc agcggttgtg cattcccagag ctgaagacaa catctacatt 900
98 gttgaagata gaccttga                                     918
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101 <211> LENGTH: 282
102 <212> TYPE: PRT
103 <213> ORGANISM: Mus musculus
105 <220> FEATURE:
106 <221> NAME/KEY: VARIANT
107 <222> LOCATION: (1)...(282)

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108 <223> OTHER INFORMATION: TIM-1, C.D2 ES-HBA and DBA/2J allele

110 <400> SEQUENCE: 3

111 Met Asn Gln Ile Gln Val Phe Ile Ser Gly Leu Ile Leu Leu Leu Pro

112 1 5 10 15

113 Gly Ala Val Asp Ser Tyr Val Glu Val Lys Gly Val Val Gly His Pro

114 20 25 30

115 Val Thr Leu Pro Cys Thr Tyr Ser Thr Tyr Arg Gly Ile Thr Thr Thr

116 35 40 45

117 Cys Trp Gly Arg Gly Gln Cys Pro Ser Ser Ala Cys Gln Asn Thr Leu

118 50 55 60

119 Ile Trp Thr Asn Gly His Arg Val Thr Tyr Gln Lys Ser Ser Arg Tyr

120 65 70 75 80

121 Asn Leu Lys Gly His Ile Ser Glu Gly Asp Val Ser Leu Thr Ile Glu

122 85 90 95

123 Asn Ser Val Glu Ser Asp Ser Gly Leu Tyr Cys Cys Arg Val Glu Ile

124 100 105 110

125 Pro Gly Trp Phe Asn Asp Gln Lys Val Thr Phe Ser Leu Gln Val Lys

126 115 120 125

127 Pro Glu Ile Pro Thr Arg Pro Pro Arg Arg Pro Thr Thr Thr Arg Pro

128 130 135 140

129 Thr Ala Thr Gly Arg Pro Thr Thr Ile Ser Thr Arg Ser Thr His Val

130 145 150 155 160

131 Pro Thr Ser Thr Arg Val Ser Thr Ser Thr Pro Pro Thr Ser Thr His

132 165 170 175

133 Thr Trp Thr His Lys Pro Asp Trp Asn Gly Thr Val Thr Ser Ser Gly

134 180 185 190

135 Asp Thr Trp Ser Asn His Thr Glu Ala Ile Pro Pro Gly Lys Pro Gln

136 195 200 205

137 Lys Asn Pro Thr Lys Gly Phe Tyr Val Gly Ile Cys Ile Ala Ala Leu

138 210 215 220

139 Leu Leu Leu Leu Val Ser Thr Val Ala Ile Thr Arg Tyr Ile Leu

140 225 230 235 240

141 Met Lys Arg Lys Ser Ala Ser Leu Ser Val Val Ala Phe Arg Val Ser

142 245 250 255

143 Lys Ile Glu Ala Leu Gln Asn Ala Ala Val Val His Ser Arg Ala Glu

144 260 265 270

145 Asp Asn Ile Tyr Ile Val Glu Asp Arg Pro

146 275 280

149 <210> SEQ ID NO: 4

150 <211> LENGTH: 849

151 <212> TYPE: DNA

152 <213> ORGANISM: Mus musculus

154 <400> SEQUENCE: 4

155 atgaatcaga ttcaagtctt catttcaggc ctcatactgc ttctcccagg cgctgtggat 60

156 tcttatgttg aagtaaagg ggtggtgggt caccctgtca cacttccatg tacttactca 120

157 acatatcgtg gaatcacaac gacatgttgg ggccgagggc aatgcccatc ttctgcttgt 180

158 caaaatacac ttatttggac caatggacat cgtgtcacct atcagaagag cagtcggtac 240

159 aacttaaagg ggcataatttc agaaggagat gtgtccttga cgatagagaa ctctgttgag 300

160 agtgacagtg gtctgtattg ttgtcgagtg gagattcctg gatggtttaa tgatcagaaa 360

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161 gtgacctttt cattgcaagt taaaccagag attcccacac gtccctccaag aagaccacaca 420
162 actacaaggc ccacagctac aggaagaccc acgactattt caacaagatc cacacatgta 480
163 ccaacatcaa ccagagtctc tacctccact cctccaacat ctacacacac atggactcac 540
164 aaaccagact ggaatggcac tgtgacatcc tcaggagata cctggagtaa tcacactgaa 600
165 gcaatccctc caggaagcc gcagaaaaac cctactaagg gcttctatgt tggcatctgc 660
166 atcgagccc tgctgctact gctccttggtg agcaccgtgg ctatcaccag gtacatactt 720
167 atgaaaagga agtcagcatc tctaagcgtg gttgccttcc gtgtctctaa gattgaagct 780
168 ttgcagaacg cagcggttgt gcattcccga gctgaagaca acatctacat tgttgaagat 840
169 agaccttga 849
171 <210> SEQ ID NO: 5
172 <211> LENGTH: 305
173 <212> TYPE: PRT
174 <213> ORGANISM: Mus musculus
176 <220> FEATURE:
177 <221> NAME/KEY: VARIANT
178 <222> LOCATION: (1)...(305)
179 <223> OTHER INFORMATION: TIM-2 BALB/c allele
181 <400> SEQUENCE: 5
182 Met Asn Gln Ile Gln Val Phe Ile Ser Gly Leu Ile Leu Leu Leu Pro
183 1 5 10 15
184 Gly Ala Val Glu Ser His Thr Ala Val Gln Gly Leu Ala Gly His Pro
185 20 25 30
186 Val Thr Leu Pro Cys Ile Tyr Ser Thr His Leu Gly Gly Ile Val Pro
187 35 40 45
188 Met Cys Trp Gly Leu Gly Glu Cys Arg His Ser Tyr Cys Ile Arg Ser
189 50 55 60
190 Leu Ile Trp Thr Asn Gly Tyr Thr Val Thr His Gln Arg Asn Ser Arg
191 65 70 75 80
192 Tyr Gln Leu Lys Gly Asn Ile Ser Glu Gly Asn Val Ser Leu Thr Ile
193 85 90 95
194 Glu Asn Thr Val Val Gly Asp Gly Gly Pro Tyr Cys Cys Val Val Glu
195 100 105 110
196 Ile Pro Gly Ala Phe His Phe Val Asp Tyr Met Leu Glu Val Lys Pro
197 115 120 125
198 Glu Ile Ser Thr Ser Pro Pro Thr Arg Pro Thr Ala Thr Gly Arg Pro
199 130 135 140
200 Thr Thr Ile Ser Thr Arg Ser Thr His Val Pro Thr Ser Thr Arg Val
201 145 150 155 160
202 Ser Thr Ser Thr Ser Pro Thr Pro Ala His Thr Glu Thr Tyr Lys Pro
203 165 170 175
204 Glu Ala Thr Thr Phe Tyr Pro Asp Gln Thr Thr Ala Glu Val Thr Glu
205 180 185 190
206 Thr Leu Pro Ser Thr Pro Ala Asp Trp His Asn Thr Val Thr Ser Ser
207 195 200 205
208 Asp Asp Pro Trp Asp Asp Asn Thr Glu Val Ile Pro Pro Gln Lys Pro
209 210 215 220
210 Gln Lys Asn Leu Asn Lys Gly Phe Tyr Val Gly Ile Ser Ile Ala Ala
211 225 230 235 240
212 Leu Leu Ile Leu Met Leu Leu Ser Thr Met Val Ile Thr Arg Tyr Val

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```

213          245          250          255
214 Val Met Lys Arg Lys Ser Glu Ser Leu Ser Phe Val Ala Phe Pro Ile
215          260          265          270
216 Ser Lys Ile Gly Ala Ser Pro Lys Lys Val Val Glu Arg Thr Arg Cys
217          275          280          285
218 Glu Asp Gln Val Tyr Ile Ile Glu Asp Thr Pro Tyr Pro Glu Glu Glu
219          290          295          300
220 Ser
221 305
224 <210> SEQ ID NO: 6
225 <211> LENGTH: 958
226 <212> TYPE: DNA
227 <213> ORGANISM: Mus musculus
229 <400> SEQUENCE: 6
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231 cctcatactg cttctccag gtgccgtgga gtctcataca gcagtgcagg ggctggcggg 120
232 tcacctgtgc acacttccat gtatttatct gacacacctt ggtggaatcg ttcctatgtg 180
233 ttggggccta ggggaatgcc gccattctta ttgtatacgg tcaacttatct ggaccaatgg 240
234 atatacggtc acacatcaga ggaacagtcg ataccagcta aaggggaata tttcagaagg 300
235 aaatgtgtcc ttgaccatag agaacactgt tgtgggtgat ggtggtcctt attgctgtgt 360
236 agtggagata cctggagcgt tccattttgt ggactatatg ttggaagtta aaccagaaat 420
237 tcccacgagt ccaccaacaa ggcccacagc tacaggaaga cccacaacta tttcaacaag 480
238 atccacacat gtaccaacat caaccagagt ctctacctct acttctccaa caccagcaca 540
239 cacagagacc taaaaccag aggccactac attttatcca gatcagacta cagctgagggt 600
240 gacagaaacc ttacctctta ctctgcaga ctggcataac actgtgacat cctcagatga 660
241 cccttgggat gataacactg aagtaatccc tccacagaag ccacagaaaa acctgaataa 720
242 gggcttctat gttggcatct ccattgcagc cctgctgata ttgatgcttc tgagcaccat 780
243 ggttatcacc aggtacgtgg ttatgaaaag gaagtcagaa tctctgagct ttgttgccct 840
244 ccctatctct aagattggag cttcccccaa aaaagtggtc gaacggacca gatgtgaaga 900
245 ccaggtctac attattgaag acactcctta cctgaagaa gagtccctagt gcctctac 958
247 <210> SEQ ID NO: 7
248 <211> LENGTH: 305
249 <212> TYPE: PRT
250 <213> ORGANISM: Mus musculus
252 <220> FEATURE:
253 <221> NAME/KEY: VARIANT
254 <222> LOCATION: (1)...(305)
255 <223> OTHER INFORMATION: TIM-2, C.D2 ES-HBA and DBA/2J allele
257 <400> SEQUENCE: 7
258 Met Asn Gln Ile Gln Val Phe Ile Ser Gly Leu Ile Leu Leu Leu Pro
259 1          5          10          15
260 Gly Ala Val Glu Ser His Thr Ala Val Gln Gly Leu Ala Gly His Pro
261          20          25          30
262 Val Thr Leu Pro Cys Ile Tyr Ser Thr His Leu Gly Gly Ile Val Pro
263          35          40          45
264 Met Cys Trp Gly Leu Gly Glu Cys Arg His Ser Tyr Cys Ile Arg Ser
265          50          55          60
266 Leu Ile Trp Thr Asn Gly Tyr Thr Val Thr His Gln Arg Asn Ser Arg
267 65          70          75          80

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VERIFICATION SUMMARY

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Output Set: N:\CRF4\03172006\J663497A.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date